

BLAST**Basic Local Alignment Search Tool**

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (19 letters)

residues 2-20 of SEQ ID No: 13

Results for: **lcl|45680** None(19aa) ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|45680

lcl|45680

Description

None

Molecule type

amino acid

Query Length

19

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#) **NEW**

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 5, 2010 4:42 AM
Number of letters	3,507,711,756
Number of sequences	10,280,272
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.368935	0.294
K	0.285947	0.11
H	1.85525	0.61

Results Statistics

Length adjustment	9
Effective length of query	10
Effective length of database	3415189308
Effective search space	34151893080
Effective search space used	34151893080

[Graphic Summary](#)

[Show Conserved Domains](#)

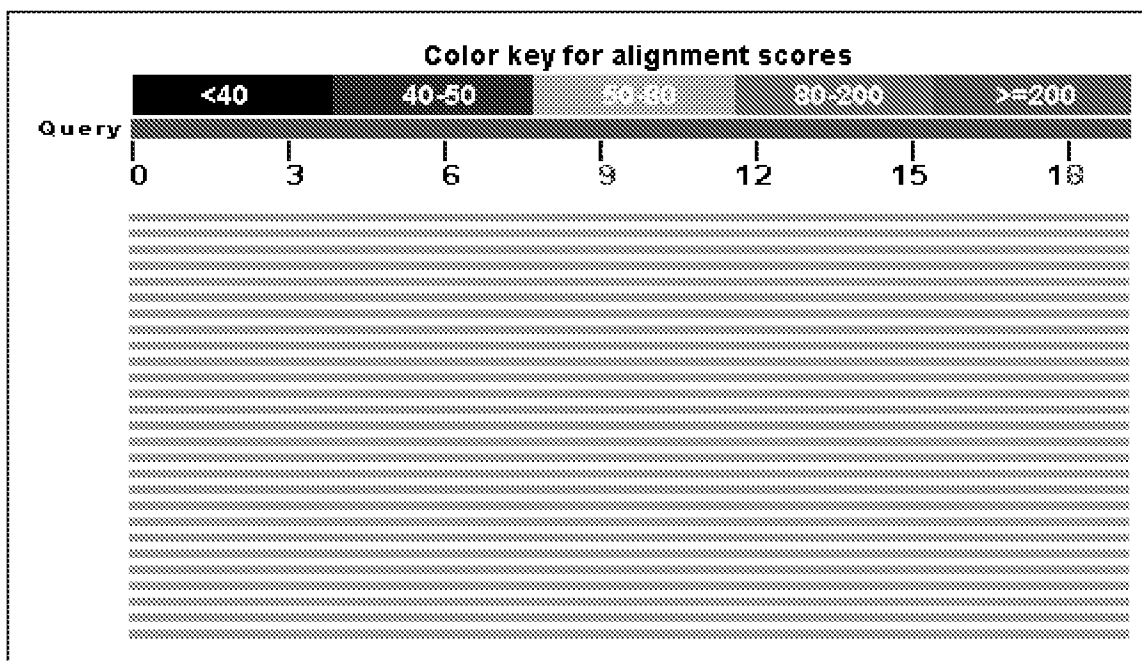
Hit the button to

See conserved domains from CDD

Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[illegible]

Descriptions

		Score	
E			
Sequences producing significant alignments:		(Bits)	Value
gb AAX59509.1	HBsAg [Hepatitis B virus]	55.4	7e-07
dbj BAG06746.1	hepatitis B surface antigen [Hepatitis B virus]	51.5	1e-05
gb ADB03191.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82752.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82751.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82750.1	large S protein [Hepatitis B virus]	50.7	2e-05
dbj BAH84154.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
dbj BAH83937.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
dbj BAH83930.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
gb ACJ66248.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66247.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66242.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66241.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66240.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66233.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66228.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66227.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66226.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66213.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66212.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66207.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66206.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66205.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66186.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66185.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66184.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66164.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66163.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66136.1	middle S protein [Hepatitis B virus] >gb ACJ66...	50.7	2e-05
gb ACJ66135.1	large S protein [Hepatitis B virus] >gb ACJ661...	50.7	2e-05
gb ACJ66130.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66129.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66128.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66122.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66096.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66095.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66081.1	large S protein [Hepatitis B virus] >gb ACJ660...	50.7	2e-05
gb ACJ66006.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66005.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66004.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ65907.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ65906.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ65859.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ65858.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ65857.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66198.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66182.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66180.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66170.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66160.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66152.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66138.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66129.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66123.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66097.1	large S protein [Hepatitis B virus] >gb ACF661...	50.7	2e-05
gb ACF66094.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACF66086.1	large S protein [Hepatitis B virus]	50.7	2e-05

gb ACR66020.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65984.1	large S protein [Hepatitis B virus]	>gb ACR661...	50.7	2e-05
gb ACR65984.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65943.1	large S protein [Hepatitis B virus]	>gb ACR659...	50.7	2e-05
gb ACR65941.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65932.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACP65923.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACP65920.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP65903.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65884.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65880.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65878.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65869.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65859.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65855.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65852.1	large S protein [Hepatitis B virus]	>gb ACR659...	50.7	2e-05
gb ACP65840.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACP65833.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACP65825.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACR65817.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65809.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65807.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACP20704.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20703.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20700.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20564.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20563.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20560.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20447.1	truncated large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20413.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20412.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20411.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20326.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20325.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20324.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20320.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20319.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20318.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20311.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20310.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACP20309.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACD03730.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACD03728.1	large S protein [Hepatitis B virus]		50.7	2e-05

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>gb|**AAX59509.1**| HBsAg [Hepatitis B virus]
Length=101

Score = 55.4 bits (123), Expect = 7e-07
Identities = 18/19 (94%), Positives = 18/19 (94%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTGQCKTCTTPAQG
Sbjct 1 GSTNTSTGQCKTCTTPAQG 19

>dbj|**BAG06746.1**| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 51.5 bits (114), Expect = 1e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG

Sbjct 73 GSTTTSTGXCKTCTTPAQG 91

>**gb|ADB03191.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACQ82752.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>**gb|ACQ82751.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>**gb|ACQ82750.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**dbj|BAH84154.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 73 GSTTTSTGPCKTCTTPAQG 91

>**dbj|BAH83937.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 73 GSTTTSTGPCKTCTTPAQG 91

>**dbj|BAH83930.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 73 GSTTTSTGPCKTCTTPAQG 91

>**gb|ACJ66248.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>**gb|ACJ66247.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACJ66242.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>**gb|ACJ66241.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>**gb|ACJ66240.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACJ66233.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACJ66228.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>**gb|ACJ66227.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>**gb|ACJ66226.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACJ66213.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>**gb|ACJ66212.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>**gb|ACJ66207.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>**gb|ACJ66206.1|** middle S protein [Hepatitis B virus]
Length=279

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 165 GSTTTSTGPCKTCTTPAQG 183

>**gb|ACJ66205.1|** large S protein [Hepatitis B virus]
Length=398

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 284 GSTTTSTGPCKTCTTPAQG 302

>**gb|ACJ66186.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)


```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 112  GSTTTTSTGPCKTCTTPAQG 130
```

>**gb|ACJ66185.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167  GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ66184.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286  GSTTTTSTGPCKTCTTPAQG 304
```

>**gb|ACJ66164.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167  GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ66163.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286  GSTTTTSTGPCKTCTTPAQG 304
```

>**gb|ACJ66136.1|** middle S protein [Hepatitis B virus]
>**gb|ACJ66178.1|** middle S protein [Hepatitis B virus]
>**gb|ACJ66192.1|** middle S protein [Hepatitis B virus]
>**gb|ACJ66198.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167  GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ66135.1|** large S protein [Hepatitis B virus]
>**gb|ACJ66177.1|** large S protein [Hepatitis B virus]
>**gb|ACJ66191.1|** large S protein [Hepatitis B virus]
>**gb|ACJ66203.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286  GSTTTTSTGPCKTCTTPAQG 304
```

>**gb|ACJ66130.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>gb|ACJ66129.1| middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTSTGPCKTCTTPAQG 185

>gb|ACJ66128.1| large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>gb|ACJ66122.1| large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>gb|ACJ66096.1| S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTSTGPCKTCTTPAQG 130

>gb|ACJ66095.1| large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>gb|ACJ66081.1| large S protein [Hepatitis B virus]
gb|ACJ66088.1| large S protein [Hepatitis B virus]
gb|ACJ66142.1| large S protein [Hepatitis B virus]
gb|ACJ66156.1| large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19
GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTSTGPCKTCTTPAQG 304

>gb|ACJ66006.1| S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTTSTGPCKTCTTPAQG 130
```

>**gb|ACJ66005.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ66004.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTTSTGPCKTCTTPAQG 304
```

>**gb|ACJ65907.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ65906.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286 GSTTTTSTGPCKTCTTPAQG 304
```

>**gb|ACJ65859.1|** S protein [Hepatitis B virus]
Length=226

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 112 GSTTTTSTGPCKTCTTPAQG 130
```

>**gb|ACJ65858.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1   GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 167 GSTTTTSTGPCKTCTTPAQG 185
```

>**gb|ACJ65857.1|** large S protein [Hepatitis B virus]
Length=400

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 286  GSTTTSTGPCKTCTTPAQG 304
```

>**gb|ACR66198.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66182.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66180.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66170.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66160.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66152.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```

>**gb|ACR66138.1|** large S protein [Hepatitis B virus]
Length=215

Score = 50.7 bits (112), Expect = 2e-05
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

```
Query 1    GSTRTSTGQCKTCTTPAQG 19
          GST TSTG CKTCTTPAQG
Sbjct 124  GSTTTSTGPCKTCTTPAQG 142
```